Package 'MLpreemption'

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Type Package

Title Maximum Likelihood Estimation of the Niche Preemption Model

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Description Provides functions for obtaining estimates of the parameter of the niche preemption model (also known as the geometric series), in particular a maximum likelihood estimator (Graffelman, 2021) <doi:10.1101/2021.01.27.428381>. The niche preemption model is a widely used model in ecology and biodiversity studies.

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Contents

Fattorini *Australian bird abudances.*

Description

The data sets consists of the names and abundances of 31 Australian birds.

Usage

```
data("Fattorini")
```

Format

A data frame with 31 observations on the following 2 variables.

`Species` a character vector

`Abundance` a numeric vector

References

Fattorini, S. (2005) A simple method to fit geometric series and broken stick models in community ecology and island biogeography. Acta Oecologica 28: pp. 199-205.

Examples

```
data(Fattorini)
```

Ganeshaiah *Indian dung beetles from Ganeshaiah et al. (1997)*

Description

The data sets consists of the names and abundances of 16 dung beetles

Usage

```
data(Ganeshaiah)
```

Format

A data frame with 16 observations on the following 2 variables.

`Species` a character vector

`Abundance` a numeric vector

References

Ganeshaiah, K.N., Chandrashekara, K. and Kuma A.R.V. (1997) Avalanche index: a new measure of biodiversity based on biological heterogeneity of the communities. Current Science 73, pp. 128-133.

Magurran, A.E. (2004) Measuring biological diversity, Blackwell Publishing, Oxford, UK.

Examples

```
data(Ganeshaiah)
```

`k_hetang` *Preemption parameter estimation by He and Tang*

Description

Calculates the He-Tang estimator for the geometric series.

Usage

```
k_hetang(x)
```

Arguments

x	A vector of counts

Value

a real number

Note

Zero counts are discarded prior to calculation of the estimator.

Author(s)

Jan Graffelman (jan.graffelman@upc.edu)

References

He, F. and Tang, D. 2008. Estimating the niche preemption parameter of the geometric series. Acta Oecologica, 33:105–107

See Also

`k_ls`,`k_ml`,`k_may`

Examples

```
data("Ganeshaiah")
x <- Ganeshaiah[,2]
k_hetang(x)
```

`k_ls` *Preemption parameter estimation by least squares regression*

Description

Calculates the least-squares estimator for the geometric series.

Usage

```
k_ls(x)
```

Arguments

`x`	A vector of ordered counts (from large to small)

Value

`khat`	estimate of the preemption parameter
`k.ll`	lower limit of the confidence interval
`k.ul`	upper limit of the confidence interval
`aic`	Akaike's information criterion
`logl`	log-likelihoood

Note

counts should be ordered from large to small.

Author(s)

Jan Graffelman (jan.graffelman@upc.edu)

References

Magurran, A. 2004. Measuring biological diversity. Blackwell Publishing, Oxford, UK.

See Also

`k_ml`,`k_hetang`,`k_may`

Examples

```
data("Ganeshaiah")
x <- Ganeshaiah[,2]
k_ls(x)
```

k_may *Preemption parameter estimation by the equation of May*

Description

Calculates the estimator of May for the geometric series.

Usage

```
k_may(xs, exclude = TRUE)
```

Arguments

xs	A vector of ordered counts
exclude	Automatically exclude zeros (if exclude=TRUE)

Details

Solves May equation by using uniroot.

Value

a real value

Note

counts should be ordered from large to small.

Author(s)

Jan Graffelman (jan.graffelman@upc.edu)

References

May, R. 1975. Patterns of species abundance and diversity. In Cody, M. and Diamond, M., editors, Ecology and Evolution of Communities, pages 81–120. Harvard Univ. Press.

See Also

k_ls,k_hetang,k_ml

Examples

```
data("Ganeshaiah")
x <- Ganeshaiah[,2]
k_may(x)
```

k_ml *Preemption parameter estimation by maximum likelihood.*

Description

Calculates the maximum likelihood estimator for the geometric series.

Usage

```
k_ml(xs, closed = FALSE, ll = 0.001, ul = 0.999)
```

Arguments

xs	A vector of ordered counts (form large to small)
closed	If closed=TRUE a closed form approximation to the ML estimator will be calculated; otherwise the exact ML estimator is calculated iteratively.
ll	Lower limit for the root searching algorithm
ul	Upper limit for the root searching algorithm

Value

a real value

Note

counts should be ordered from large to small.

Author(s)

Jan Graffelman (jan.graffelman@upc.edu)

References

Graffelman, J. (2021) Maximum likelihood estimation of the geometric niche preemption model.

See Also

k_ls,k_hetang,k_may

Examples

```
data("Ganeshaiah")
x <- Ganeshaiah[,2]
k_ml(x)
```

Mehrabi *Costa Rica dung beetle counts from Mehrabi et al. (2014)*

Description

The data sets consists of the names and total abundances of 31 dung beetles along 16 transects (A, B, ... P). Transects A, C, ..., O used randomly placed traps (control), whereas transects B, D, ..., P used microhabitat standardized traps (treatment).

Usage

```
data("Mehrabi")
```

Format

A data frame with 31 observations on the following 16 variables.

`A` a numeric vector

`B` a numeric vector

`C` a numeric vector

`D` a numeric vector

`E` a numeric vector

`F` a numeric vector

`G` a numeric vector

`H` a numeric vector

`I` a numeric vector

`J` a numeric vector

`K` a numeric vector

`L` a numeric vector

`M` a numeric vector

`N` a numeric vector

`O` a numeric vector

`P` a numeric vector

References

Mehrabi, Z., Slade, E.M., Solis, A. and Mann, D.J. (2014) The Importance of Microhabitat for Biodiversity Sampling (2014) PLoS ONE 9(12) e114015. doi 10.1371/journal.pone.0114015

Examples

```
data(Mehrabi)
```

`preemption.fit` *Estimation of the preemption parameter of a geometric series by various methods*

Description

Function `preemption.fit` can estimate the preemption parameter of a geometric series by four specifici methods, or list all estimates simultaneously for comparison.

Usage

```
preemption.fit(x, method = "ml", closed = FALSE, verbose = TRUE)
```

Arguments

`x`	Vector of counts (abundances of species)
`method`	Estimation method ("ml" = maximum likelihood, "ls" = least squares, "May" = May's equation, "HT" = He-Tang's equation, "all" = lists all four estimators)
`closed`	If `closed=FALSE` the exact value of the ML estimator will be calculated by iteration, if `closed=TRUE` a good closed-form approximation is given
`verbose`	The function is silent if `verbose=FALSE` or prints results if `verbose=TRUE`

Value

`khat`	the estimate of the preemption parameter
`ll`	lower limit of 95 confidence interval
`ul`	upper limit of 95 confidence interval

Author(s)

Jan Graffelman (jan.graffelman@upc.edu)

References

Graffelman, J. (2021) Maximum likelihood estimation of the geometric niche preemption model

See Also

`preemption.t`

Examples

```
data(Ganeshaiah)
preemption.fit(Ganeshaiah[,2])
```

preemption.t *Preemption t test*

Description

Function preemption.t implements a t test for comparing the preemption parameters of the geometric series for two samples.

Usage

```
preemption.t(x1, x2, verbose = TRUE)
```

Arguments

x1	Species counts for the first sample
x2	Species counts for the second sample
verbose	The function is silent if verbose=FALSE or prints results if verbose=TRUE

Value

Tstat	The t statistic
df	The degrees of freedom
pval	The p-value of the test

Author(s)

Jan Graffelman (jan.graffelman@upc.edu)

References

Graffelman, J. (2021) Maximum likelihood estimation of the geometric niche preemption model

See Also

preemption.fit

Examples

```
data(Mehrabi)
x <- sort(Mehrabi[,1],decreasing=TRUE)
y <- sort(Mehrabi[,2],decreasing=TRUE)
results <- preemption.t(x,y)
```

raplot *Rank-abundance plot*

Description

Function raplot creates a rank-abundance plot online, and can show decaying lines fitted by various method.

Usage

```
raplot(x, xlab = "Species rank", ylab = "log (Relative abundance)",
     main = "Rank-Abundance plot", reflines = c(1, 2, 3, 4), alpha = 0.05, leg = FALSE)
```

Arguments

x	Vector of counts (species abundances)
xlab	Label for the x axis
ylab	Label for the y axis
main	Title for the plot
reflines	Lines to be drawn in the plot: 1=ML, 2=LS, 3=May, 4=He-Tang
alpha	Signifance level (0.05 by default)
leg	Show legend leg=TRUE or not leg=FALSE

Value

NULL

Author(s)

Jan Graffelman (jan.graffelman@upc.edu)

References

Graffelman, J. (2021) Maximum likelihood estimation of the geometric niche preemption model

Examples

```
data(Fattorini)
raplot(Fattorini[,2])
```

raplot.paired *Rank-abundance plot for two samples*

Description

Function raplot.paired creates a rank-abundance plot on screen, and can show decaying lines with uncertainty zones for two samples fitted by maximum likelihood.

Usage

```
raplot.paired(x, y, xlab = "Species rank", ylab = "log (Relative abundance)",
              main = "Rank-abundance", sym = c(1, 2), alpha = 0.05)
```

Arguments

x	Count vector of the first sample
y	Count vector of the second sample
xlab	Label x axis
ylab	Label y axis
main	Main title for the plot
sym	Symbols for first and second sample (c(1,2) by default)
alpha	Significance level (0.05 by default)

Value

NULL

Author(s)

Jan Graffelman (jan.graffelman@upc.edu)

References

Graffelman, J. (2021) Maximum likelihood estimation of the geometric niche preemption model

See Also

raplot

Examples

```
data("Mehrabi")
raplot.paired(Mehrabi[,1],Mehrabi[,2])
```

Index